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SEQUENCE LISTING

3

<110> Millennium Pharmaceuticals, Inc.
Meyers, Rachel

<120> 47324, A NOVEL HUMAN G-PROTEIN AND USES
THEREFOR

<130> 38155-20035.00

<140> US 09/945,173

<141> 2001-08-31

<150> US 60/229,293

<151> 2000-09-01

<160> 11

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<210> 1

<211> 1694

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (19)...(729)

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ttg	gga	gac	tca	ggt	gtt	ggg	aaa	tct	tcg	tta	gtc	cat	ctc	cta	tgc	99
Leu	Gly	Asp	Ser	Gly	Val	Gly	Lys	Ser	Ser	Leu	Val	His	Leu	Leu	Cys	
		15				20						25				

caa	aat	caa	gtg	ctg	gga	aat	cca	tca	tgg	act	gtg	ggc	tgc	tca	gtg	147
Gln	Asn	Gln	Val	Leu	Gly	Asn	Pro	Ser	Trp	Thr	Val	Gly	Cys	Ser	Val	
		30				35					40					

gat	gtc	aga	gtt	cat	gat	tac	aaa	gaa	gga	acc	cca	gaa	gag	aag	acc	195
Asp	Val	Arg	Val	His	Asp	Tyr	Lys	Glu	Gly	Thr	Pro	Glu	Glu	Lys	Thr	
		45				50					55					

tac	tac	ata	gaa	tta	tgg	gat	gtt	gga	ggc	tct	gtg	ggc	agt	gcc	agc	243
Tyr	Tyr	Ile	Glu	Leu	Trp	Asp	Val	Gly	Gly	Ser	Val	Gly	Ser	Ala	Ser	
		60				65				70					75	

agc	gtg	aaa	agc	aca	aga	gca	gta	ttc	tac	aac	tcc	gta	aat	ggc	att	291
Ser	Val	Lys	Ser	Thr	Arg	Ala	Val	Phe	Tyr	Asn	Ser	Val	Asn	Gly	Ile	
				80						85					90	

att	ttc	gta	cac	gac	tta	aca	aat	aag	aag	tcc	tcc	caa	aac	ttg	cgt	339
Ile	Phe	Val	His	Asp	Leu	Thr	Asn	Lys	Lys	Ser	Ser	Gln	Asn	Leu	Arg	

95	100	105	
cgt tgg tca ttg gaa gct ctc aac agg gat ttg gtg cca act gga gtc			387
Arg Trp Ser Leu Glu Ala Leu Asn Arg Asp Leu Val Pro Thr Gly Val			
110	115	120	
ttg gtg aca aat ggg gat tat gat caa gaa cag ttt gct gat aac caa			435
Leu Val Thr Asn Gly Asp Tyr Asp Gln Glu Gln Phe Ala Asp Asn Gln			
125	130	135	
ata cca ctg ttg gta ata ggg act aaa ctg gac cag att cat gaa aca			483
Ile Pro Leu Leu Val Ile Gly Thr Lys Leu Asp Gln Ile His Glu Thr			
140	145	150	155
aag cgc cat gaa gtt tta act agg act gct ttc ctg gct gag gat ttc			531
Lys Arg His Glu Val Leu Thr Arg Thr Ala Phe Leu Ala Glu Asp Phe			
160	165	170	
aat cca gaa gaa att aat ttg gac tgc aca aat cca cgg tac tta gct			579
Asn Pro Glu Glu Ile Asn Leu Asp Cys Thr Asn Pro Arg Tyr Leu Ala			
175	180	185	
gca ggt tct tcc aat gct gtc aag ctc agt agg ttt ttt gat aag gtc			627
Ala Gly Ser Ser Asn Ala Val Lys Leu Ser Arg Phe Phe Asp Lys Val			
190	195	200	
ata gag aag aga tac ttt tta aga gaa ggt aat cag att cca ggc ttt			675
Ile Glu Lys Arg Tyr Phe Leu Arg Glu Gly Asn Gln Ile Pro Gly Phe			
205	210	215	
cct gat cgg aaa aga ttt ggg gca gga aca tta aag agc ctt cat tat			723
Pro Asp Arg Lys Arg Phe Gly Ala Gly Thr Leu Lys Ser Leu His Tyr			
220	225	230	235
gac tga attacactca tcctttggaa gagtgagcaa gcagtggcag tttttcacag			779
Asp *			
ctcatcttgc tgtgttcaat tattaccatc acagcctttt aacaaaaatca tcttaaaatg			839
ctacccttca gccttaccct ttaatggaaa aatgaaagga agtgacaata cgggaggtcc			899
aaactttgtc cctgttctct gtgttcctta cctttctgtc cctgtgtata gattatgtaa			959
aagccttgtg taaatatgag atgttgtcaa aatgatgcag taaatgagca atgacagtgt			1019
actgcagaga aaatttactc ttgcctagaa ctggagggtt tttatgggtc tgtaattttc			1079
ccacactcat tgctgaaagc ttaattaagt acttcaaaaa cgtatctcca ttgttttacc			1139
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tgccataata tagcaaccct tgtctccctc ttctctcctt tgcaaatggc tcagtgactg			1319
gaagaggcgg actaatagcc agagttaa ataaatacaa attaataata catagagaac			1379
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<210> 2

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<212> PRT
 <213> Homo sapiens

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 20 25 30
 Gly Asn Pro Ser Trp Thr Val Gly Cys Ser Val Asp Val Arg Val His
 35 40 45
 Asp Tyr Lys Glu Gly Thr Pro Glu Glu Lys Thr Tyr Tyr Ile Glu Leu
 50 55 60
 Trp Asp Val Gly Gly Ser Val Gly Ser Ala Ser Ser Val Lys Ser Thr
 65 70 75 80
 Arg Ala Val Phe Tyr Asn Ser Val Asn Gly Ile Ile Phe Val His Asp
 85 90 95
 Leu Thr Asn Lys Lys Ser Ser Gln Asn Leu Arg Arg Trp Ser Leu Glu
 100 105 110
 Ala Leu Asn Arg Asp Leu Val Pro Thr Gly Val Leu Val Thr Asn Gly
 115 120 125
 Asp Tyr Asp Gln Glu Gln Phe Ala Asp Asn Gln Ile Pro Leu Leu Val
 130 135 140
 Ile Gly Thr Lys Leu Asp Gln Ile His Glu Thr Lys Arg His Glu Val
 145 150 155 160
 Leu Thr Arg Thr Ala Phe Leu Ala Glu Asp Phe Asn Pro Glu Glu Ile
 165 170 175
 Asn Leu Asp Cys Thr Asn Pro Arg Tyr Leu Ala Ala Gly Ser Ser Asn
 180 185 190
 Ala Val Lys Leu Ser Arg Phe Phe Asp Lys Val Ile Glu Lys Arg Tyr
 195 200 205
 Phe Leu Arg Glu Gly Asn Gln Ile Pro Gly Phe Pro Asp Arg Lys Arg
 210 215 220
 Phe Gly Ala Gly Thr Leu Lys Ser Leu His Tyr Asp
 225 230 235

<210> 3
 <211> 711
 <212> DNA
 <213> Homo sapiens

<400> 3
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 tcgttagtcc atctcctatg ccaaaatcaa gtgctgggaa atccatcatg gactgtgggc 120
 tgctcagtgg atgtcagagt tcatgattac aaagaaggaa cccagaaga gaagacctac 180
 tacatagaat tatgggatgt tggaggctct gtgggcagtg ccagcagcgt gaaaagcaca 240
 agagcagtat tctacaactc cgtaaatggg attattttcg tacacgactt aacaaataag 300
 aagtcctccc aaaacttgcg tcgttgggtca ttggaagctc tcaacaggga tttggtgcca 360
 actggagtct tgggtgacaaa tggggattat gatcaagaac agtttgctga taaccaata 420
 ccactgttgg taatagggac taaactggac cagattcatg aaacaaagcg ccatgaagtt 480
 ttaactagga ctgcttttct ggctgaggat ttcaatccag aagaaattaa tttggactgc 540
 acaaatccac ggtacttagc tgcaggttct tccaatgctg tcaagctcag taggtttttt 600
 gataaggtca tagagaagag atacttttta agagaaggta atcagattcc aggttttctt 660
 gatcggaaaa gatttggggc aggaacatta aagagccttc attatgactg a 711

<210> 4
 <211> 191
 <212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 4

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Lys	Glu	Met	Arg	Ile	Leu	Ile	Leu	Gly	Leu	Asp	Asn	Ala	Gly	Lys	Thr	
			20					25					30			
Thr	Ile	Leu	Tyr	Lys	Leu	Lys	Leu	Gly	Glu	Ile	Val	Thr	Thr	Ile	Pro	
		35					40					45				
Thr	Ile	Gly	Phe	Asn	Val	Glu	Thr	Val	Glu	Tyr	Lys	Asn	Ile	Lys	Phe	
	50					55					60					
Thr	Val	Trp	Asp	Val	Gly	Gly	Gln	Glu	Ser	Leu	Arg	Pro	Leu	Trp	Arg	
65					70					75					80	
Asn	Tyr	Phe	Pro	Asn	Thr	Asp	Ala	Val	Ile	Phe	Val	Val	Asp	Ser	Ala	
				85					90					95		
Asp	Arg	Glu	Arg	Ile	Glu	Glu	Ala	Lys	Glu	Glu	Leu	His	Ala	Leu	Leu	
			100					105					110			
Asn	Glu	Glu	Glu	Leu	Ala	Asp	Ala	Pro	Leu	Leu	Ile	Phe	Ala	Asn	Lys	
	115						120						125			
Gln	Asp	Leu	Pro	Gly	Ala	Met	Ser	Glu	Ala	Glu	Ile	Arg	Glu	Ala	Leu	
	130					135						140				
Gly	Leu	His	Glu	Leu	Lys	Gly	Ser	Lys	Gly	Lys	Val	Thr	Leu	Glu	Gly	
145					150					155					160	
Asp	Arg	Pro	Trp	Glu	Ile	Gln	Gly	Cys	Ser	Ala	Val	Lys	Gly	Glu	Gly	
				165					170					175		
Leu	Tyr	Glu	Gly	Leu	Asp	Trp	Leu	Ser	Asn	Asn	Ile	Lys	Lys	Arg		
			180					185						190		

<210> 5

<211> 198

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 5

Lys	Leu	Val	Leu	Ile	Gly	Asp	Ser	Gly	Val	Gly	Lys	Ser	Ser	Leu	Leu	
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Ile	Arg	Phe	Thr	Asp	Asn	Lys	Phe	Val	Glu	Glu	Tyr	Ile	Pro	Thr	Ile	
			20					25					30			
Gly	Val	Asp	Phe	Tyr	Thr	Lys	Thr	Val	Glu	Val	Asp	Gly	Lys	Thr	Val	
		35					40					45				
Lys	Leu	Gln	Ile	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Arg	Phe	Arg	Ala	Leu	
	50					55					60					
Arg	Pro	Ala	Tyr	Tyr	Arg	Gly	Ala	Gln	Gly	Phe	Leu	Leu	Val	Tyr	Asp	
65					70					75					80	
Ile	Thr	Ser	Arg	Asp	Ser	Phe	Glu	Asn	Val	Lys	Lys	Trp	Leu	Glu	Glu	
				85					90					95		
Ile	Leu	Arg	His	Ala	Asp	Lys	Asp	Glu	Asn	Val	Pro	Ile	Val	Leu	Val	
			100					105					110			
Gly	Asn	Lys	Cys	Asp	Leu	Glu	Asp	Asp	Glu	Asp	Leu	Glu	Leu	Thr	Glu	
		115					120					125				
Gly	Gln	Lys	Arg	Val	Val	Ser	Thr	Glu	Glu	Gly	Glu	Ala	Leu	Ala	Lys	

130		135		140											
Glu	Leu	Gly	Ala	Leu	Pro	Phe	Met	Glu	Thr	Ser	Ala	Lys	Thr	Asn	Thr
145					150					155					160
Asn	Val	Glu	Glu	Ala	Phe	Glu	Glu	Leu	Ala	Arg	Glu	Ile	Leu	Lys	Lys
				165					170						175
Val	Ser	Glu	Val	Asn	Val	Asn	Leu	Asp	Gln	Pro	Ala	Lys	Lys	Lys	Lys
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Ser	Lys	Cys	Cys	Ile	Leu										
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<210> 6
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 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

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Phe Tyr Asp Leu Asn Ser Asp Trp Arg Met Cys Arg Gln Gln Arg Glu
35 40 45
Ser Phe Tyr Lys Asn Ile Asp Gly Ile Val Leu Val Tyr Asn Met Leu
50 55 60
Glu Leu Ser Ser Gln Asp Ser Leu His Asp Trp Leu Tyr Asp Pro Leu
65 70 75 80
Arg Gln Ile Cys Lys His Arg His Leu Arg Ile Arg Ser Ile Leu Lys
85 90 95
Asn His Asn Ala Pro Ile Leu Val Val Gly Thr Asn Leu Asp Lys Leu
100 105 110
Met Arg Arg Pro Leu Arg Arg Arg Gly Ser Ile Ala His Gln Leu Asn
115 120 125
Val Glu Glu Met Leu Val Asn Cys Leu Asp Pro Gln Ser Phe Val Asp
130 135 140
Lys Ser Arg Asn Gln Gly Lys Leu Tyr Gly Phe Leu Asn Arg Val Ile
145 150 155 160
Glu Phe Lys Glu Gln Phe
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<210> 7
 <211> 50
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

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Val Arg Ile Leu Met Leu Gly Asp Arg Gly Val Gly Lys Thr Ser Leu
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Thr Asn Leu Met Ala Thr Thr Glu Ile Thr Pro Thr Pro Asp Ser Arg
20 25 30
Thr Val Gly Glu Glu Ser Trp His Val Gln Val Arg Leu His Glu Tyr
35 40 45

Ser Lys
50

<210> 8
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<400> 8
Thr Asp Asn Leu Gly Thr Asp Gly His Ile Leu Phe Asp Met Glu Glu
1 5 10 15
Phe Leu Gly Ala Thr Gln Thr Pro Ile Leu Val Met Gly Thr Lys Leu
20 25 30
Asp Leu Leu Asp Glu Lys Arg His Pro Lys Met Gly Val Lys Lys Pro
35 40 45
Gly Gly Ile Ala Asp Lys Cys Gly Ala Glu Glu Ile Trp Leu Asn Cys
50 55 60
Arg Asn Ser Arg Ser Leu Ala Ala Gly Thr Thr Asp Ala Val Lys Leu
65 70 75 80
Ser Arg Phe Phe Asp Arg Val Ile Glu Asn Arg Lys Ala Leu Arg Ala
85 90 95
Ala Leu Ala Phe Gly Val Ser Ser Ser Asn Ala Val Ser Pro Pro Asp
100 105 110
Arg Arg Arg Phe Gly Pro Thr Ser Ala Lys
115 120

<210> 9
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

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Gln Val Arg Val Leu Val Val Gly Asp Ser Gly Val Gly Lys Thr Ser
1 5 10 15
Leu Val His Leu Ile Asn Lys Gly Ser Ser Ile Val Arg Pro Pro Gln
20 25 30
Thr Ile Gly Cys Thr Val Gly Val Lys His Ile Thr Tyr Gly Ser Pro
35 40 45
Ala Ser Ser Ser Ser Ile Gln
50 55

<210> 10
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

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Lys Ile Val Ile Ile Gly Asp Ser Gly Val Gly Lys Thr Ser Leu Leu

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			20					25					30			
Thr	Thr	Arg	Thr	Val	Val	Asp	Ser	Tyr	Lys	Ser	Thr	Ile	Gly	Val	Asp	
		35					40					45				
Phe	Asn	Val	Lys	Thr	Thr	Ile	Glu	Val	Val	Asp	Thr	Asp	Gly	Lys	Asn	
	50					55					60					
Ile	Lys	Leu	Gln	Ile	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Arg	Tyr	Arg	Ser	
65					70				75					80		
Met	Leu	Thr	Ser	Met	Glu	Ala	Tyr	Tyr	Arg	Gly	Ala	Glu	Ala	Asp	Ile	
			85					90						95		
Ile	Val	Tyr	Asp	Val	Asp	Ser	Ser	Glu	Ser	Ser	Phe	Glu	Asn	Gln	Thr	
			100					105					110			
Lys	Trp	Leu	Lys	Glu	Ile	Leu	Arg	His	Ala	Ser	Asn	Glu	Glu	Ala	Ser	
	115					120					125					
Glu	Asn	Val	Pro	Ile	Ile	Leu	Val	Gly	Asn	Lys	Ala	Asp	Leu	Glu	Val	
	130					135					140					
Pro	Asn	Pro	Glu	Glu	Val	Glu	Glu	Glu	Lys	Glu	Glu	Ala	Ser	Thr	Glu	
145					150					155					160	
Glu	Glu	Ala	Gln	Ser	Phe	Ala	Glu	Glu	Lys	Gly	Leu	Gly	Val	Val	Pro	
			165					170						175		
Phe	Ile	Glu	Thr	Ser	Ala	Lys	Thr	Thr	Gly	Thr	Asn	Val	Glu	Glu	Val	
			180					185					190			
Phe	Gln	Glu	Leu	Val	Arg	Glu	Ile	Leu	Lys	Lys	Lys	Lys	Glu	Ile	Gln	
	195					200						205				
Glu	Lys	Ala	Asp	Gln	Glu	Lys	Tyr									
	210					215										

<210> 11

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid consensus sequence

<221> VARIANT

<222> (1)...(29)

<223> Xaa = Any Amino Acid

<400> 11

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Asp	Leu	Ile	Val	Xaa	Xaa	Ser	Thr	Gly	Xaa	Thr	Leu	Met				
			20					25								